

We then propose to use this powerful avenue



Application to Synthesis Centre of Biodiversity Sciences (sDiv)

Working group proposal

Biodiversity Dynamics – The Nexus Between Space & Time

Acronym: sEcoEvo

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Public summary: Biodiversity is critical for providing ecosystem services and sustaining functioning ecosystems, yet we lack a robust understanding of the relative roles of ecological and evolutionary processes in its origins and maintenance. Participants with expertise at the intersection of macroecology, population genomics, and phylogenetics, will develop an integrative and predictive theoretical framework. The work synthesizes data from plants, insects, and vertebrates, geology, and climate, and uses natural experiments provided by insular systems replicated across snapshots of ecological to evolutionary time.

Submission date: 14/02/2017

1 General information

Table 1: Key data of proposed working group. <Please complete the table listed.>

Working group title	
Acronym	sEcoEvo
Keywords (up to 5 words/terms)	Macroecology, population genomics, chronosequence neutral theory, maximum entropy
Name of 1st applicant (name and surname)	Rosemary G Gillespie
Name of 2nd applicant (if applicable)	Michael Hickerson
Total working group costs (incl. all meetings; excl. PostDoc)	31,170
No. of Meetings	2
Are you applying for a Working Group -Postdoc (yes/no)?	No
Who are/is the iDiv contact(s) among the participants (name and surname)?	Jonathan Chase, Tiffany Knight

2 Project summary

A central challenge in understanding the origins of biodiversity is that, while we can observe and test local ecological phenomena, we must usually infer the longer-term outcomes of these ecological forces indirectly. We propose to develop inferential models at the interface between macroecology and population-level processes, and apply them to data from geological or ecological chronosequences that present communities of different ages. Inferences from these “snapshots in time” thereby allow for model validation and a link between direct observational methods for local communities and models that make indirect inferences underlying community history. The workshop will use data from multiple insular systems, each comprising replicated sites that range from <500 to >5 million years. We propose to directly link ecological theories and models of community composition and comparative population genetics, all within a temporal framework. Our approach is to look for general patterns that emerge from theories of statistical mechanics, and then build a unified model bridging theory from phylogenetic and comparative population genetics with ecological theory, so as to understand the history underlying patterns of species diversity. This model will then be used to make joint predictions of species abundances and genetic diversities over time. We will then test this model with data collected across diverse taxa and a range of systems that provide snapshots in time. This unified approach will bridge ecological and evolutionary theory to elucidate processes responsible for origins and maintenance of species diversity and provide a framework for making predictions about biodiversity dynamics.

3 List of abbreviations

SDM – species distribution modelling	METE – Maximum Entropy Theory of Ecology
SAD – Species Abundance Distribution	NSF – National Science Foundation (USA)

4 State of the art and theoretical context

The biological diversity we see today has been produced through a complex of mechanisms that have acted over past geological and climatological periods as well as today. Despite recognition of past influences, the conceptual constructs and associated data for linking historical theories of evolution and demography with the biodiversity metrics used by macroecologists, remain enigmatic. Much needed is a means to reconcile the interaction of deterministic and neutral processes underlying multiple levels of biodiversity that span metrics of richness and abundance [22, 26] to spatial patterns of genetic diversity [8]. Inference of community assembly developed by coupling phylogenetic hypotheses with ecological data from extant taxa have been useful [4, 21], yet these approaches lack a link between community-level processes and within-species variation, which could reveal and exploit the detailed population processes underlying assembly. Although population genetics and phylogeography have always had enormous potential for the inference of community expansion and assembly in the general context of climatological change, these studies suffer from the high uncertainty surrounding limited numbers of genetic markers [2], overly generic models [17], ignoring spatial processes [12], and confounding effects of spatial patterns of adaptation [7]. Although population genomic historical inference have benefitted from recent advances in spatial methods [18], as well as ever more powerful genome-scale approaches [25], testing community-scale hypotheses with multi-taxa data could be profoundly improved and enriched if models were grounded in macroecological and biogeographic theory. Conversely, it is well recognized that models in community ecology have been overly reliant on species abundance distributions which are by themselves often insufficient for distinguishing competing models of assembly without adding other dimensions of data [11]. Specifically it has been suggested that coupling population genomics with neutral (i.e., stochastic) and deterministic (e.g., niche-filtering, competition) models of community assembly could enable a whole new type of inference [10]. Each of these research areas is rich in theory upon which we can build. Although traditionally used to infer historical processes at different scales, combining models of species abundance distributions with complementary models of spatiotemporal distributions of population genomic data, could provide a powerful unified approach for developing joint predictions under alternative assembly models and subsequently testing these predictions with joint time series data.

5 Aims and scope of the working group

Topic: "Next generation mechanistic modelling for biodiversity research"

Overarching goals. We propose a unified approach bridging theory from phylogenetic and comparative population genomics with ecological theory (focusing on the most developed neutral theory of biodiversity and biogeography but with easy extension to other growing areas of research such as maximum entropy theory). We will then apply this theory to diverse sets of data, each providing information on communities across a spectrum of ecological and

evolutionary time. This approach will provide a dynamic framework for the study of community ecology, which tends to view species as a fairly static pool [13] and will also give us new opportunities to understand why certain biodiversity patterns consistently emerge, such as recurrent shapes of species abundance distributions and species area relationships [11, 14]. Are these patterns all linked to the same set of universal mechanisms or are these emergent properties idiosyncratic with respect to each other? Could adding additional axes of information be key to distinguishing processes that are unidentifiable from ecological metrics alone? By unifying macro-ecological parameters with those that underpin community-level phylogenetic and population genomic data, we intend to develop a joint inferential framework that incorporates spatial and temporal non-equilibrium processes.

The data we will use for testing this unified approach have one thing in common - they have all been collected from systems that are discrete and geographically isolated, with sites that are replicated across age gradients ranging from <500 years to > 5 million years old. Thus, each system provides data on community assembly over ecological to evolutionary time. In an effort to explain commonalities in the origins and assembly patterns of biodiversity, we will iterate the development of models and testing them on the different sets of data, asking the question, how do ecological processes (colonization/ fitting, etc) give way to evolutionary processes (adaptation/ specialization, etc) in the community as a whole? Specific questions include: How do processes such as colonization, species turnover, and genetic cohesion give way to priority effects and genetic differentiation over time? How does beta diversity change over time, and how do communities reach steady state (if they do) - what time frame and in what taxa? What is the relative importance of stochastic vs ecologically deterministic processes in shaping species diversity?

Of the participants, 12 bring a theoretical perspective, each developing approaches at the eco-evolutionary boundary. Several bring expertise derived from ecological perspectives, including **Chase, Rominger, Rosindell, Hortal, McGill, Kiel**; also **Graham** in the context of SDMs. Others bring theory from a more evolutionary perspective, **Hickerson, Harmon, Massol, Overcast, Etienne**. Other participants have a strong background in specific systems, using data to address questions at the eco-evolutionary boundary – **Gillespie**, arthropods in the Hawaiian and Pacific islands; **Knight**, Hawaiian plants; **Emerson**, arthropods in the Canaries, Azores, Mascarenes; **Parent**, invertebrates in the Galapagos; **Wagner**, cichlid fish in African rift lakes; **Mahler**, Caribbean lizards; and **Graham**, hummingbirds in sky islands.

Synergies & integration. Primary synergies are (1) Integrating ecological and evolutionary approaches into a dynamic framework to provide insights into how properties of communities and their component lineages are shaped and evolve. (2) Determining commonalities in assembly of communities that span organismic diversity (arthropods, plants, vertebrates) in diverse systems.

Synthetic aspect Our aim is to develop a general understanding of how taxa assemble over the temporal boundary that characterizes ecological *vs.* evolutionary processes. The use of diverse data within an integrated theoretical construct, will allow us to achieve this goal.

5.1 Scientific objectives

We propose to address the questions outlined above using a 4-pronged approach: (a)

Community metrics: Communities are complex and processes underlying them ever-changing. A first step to understanding these processes is to determine whether the patterns used to describe given community (e.g. species abundance distribution, species area relationship, network topology) deviate from statistical steady state [6], implicating additional causal processes, such as biological disturbances or the evolution of specialization [19]. Thus a theory predicting statistical steady state can serve as a null model to filter out patterns and communities that might show interesting mechanistic processes in the act of playing out and warranting further detailed modelling and study. Such a theory has been developed based on maximizing information entropy [6]; while the biological mechanisms that might generate such state variables are unknown, we do know that the general shapes of macroecological metrics are dictated by these state variables [9]. However, this maximum entropy theory of ecology is, by design, entirely static (focus is at one point in time). By looking across insular systems of different age, we can identify communities that fall outside statistical steady state and identify drivers (e.g. elevated rates of niche evolution, see objective [c]). (b) **Population**

differentiation & species diversity through time. To date, most studies of population differentiation and species diversification are reconstructed using extant taxa with molecular phylogenies to generate lineage-through-time plots and estimate diversification rates [15]. The challenge is how to estimate the nature of the species pool involved in early diversification [5]. Habitat chronosequences provide a way around this. The mathematics necessary to bridge phylogenies and chronosequences depends again on building hierarchical models of birth-death processes allowing the patterns seen in each discrete habitat to influence the rates of speciation, extinction and immigration.

(c) **Niche evolution through time.** Understanding of niche evolution provides insights into how species' attributes are modified through selection, including the role of convergent evolution and degree of trait lability [16]. To determine how niche traits evolve over time, most work has focused on extant taxa with phylogenetic hypotheses to infer shifts in distribution associated with landscape change [3] and rates of trait evolution [23]. Here again, extant species at a single time slice can be misleading [24]. We will be using comparative phylogenetic and population genomic methods coupled with multi-taxa SDMs and community assembly models in different systems of spatially or temporally discrete habitats of different ages. (d) **Linking models of community assembly and population genomics** (Fig. 1). With both of these areas rich in theory, explicit links could potentially enable a whole new type of inference. These two bodies of

theory are traditionally used to infer historical processes at different scales, yet the temporal and spatial dynamics of species abundances and species presence/absence that parameterize models of community assembly could be scaled into variables that are quantifiable with population genomic inference. Under this unified model, one could jointly use abundance data and aggregate population genomic data to test alternative models of assembly that have been previously intractable with relative abundance data alone. So far we have implemented this unified model in the *gimmeSADπ* simulation pipeline (publicly available on github) by merging an individual-based forward time community dispersal model [20] with a backwards-time hierarchical multi-taxa coalescent model using the msPrime coalescent simulator.

5.2 Deliverables

These are described in the work plan below.

6 Work plan

Pre-meeting plans and deliverables

- a) Invited manuscript for *Trends in Ecology and Evolution* lead by A. J. Rominger addressing how combining ecological theory with next generation community-wide sequencing data can be used to identify communities out of steady state.

- b) *gimmeSADπ* simulation pipeline lead by I. Overcast and M. Hickerson designed to jointly estimate parameters of neutral molecular evolution and neutral community ecology using next generation metabarcoding mtDNA data.
- c) Bayesian hierarchical modelling approach lead by A. J. Rominger to provide robust estimates of real abundances from next generation metabarcoding data
- d) Arthropod community composition, population genomics, and barcoding reference library for the Hawaiian Islands resulting from an NSF Dimensions in Biodiversity lead by R. G. Gillespie
- e) Analysis of extensive vegetation plot data across the Hawaiian Islands using the maximum entropy theory of ecology, lead by A.J. Rominger and J. Chase

Working group deliverables

- a) Synthesis of patterns of deviation from statistical steady state (as quantified by METE) across island systems with known chronologies and across taxonomic groups

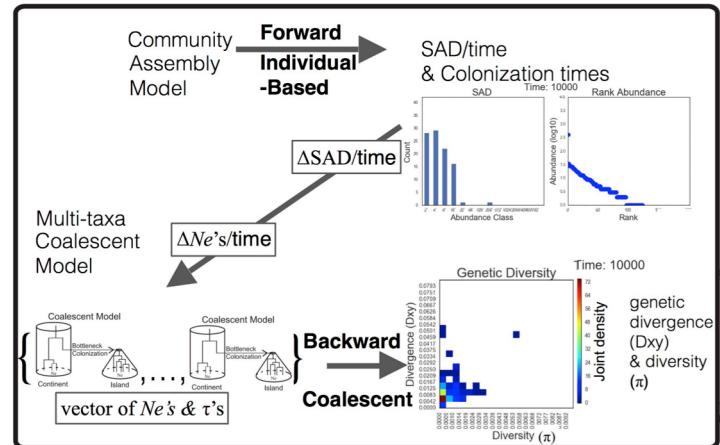


Figure 1. *GimmeSADπ* joint population genetic/community assembly model. The forward time model involves island assembly generating local abundance distributions over time with variable colonization times. The temporally dynamic local abundances are re-scaled into N_e distributions to generate multi-species genetic data under the coalescent summarized here with a time dependent joint spectrum of genetic diversity statistics.

- b) Characterization of evolutionary changes in niche occupancy and niche partitioning across chronosequences.
- c) Characterization of the relationship between deviations from METE and demographic/genetic parameters inferred from *gimmeSAD*
- d) Synthesis of demographic/genetic parameters from *gimmeSAD*, deviations from METE and inference of niche evolution from multi species distribution models across chronosequences.
- e) Developing and implementing Bayesian hierarchical model that jointly parameterizes assembly models with community population historical demography and associated community ecological metrics, phylogenetic metrics and multi-taxon next generation population genomic data summarizations.

Currently, the *gimmeSADn* simulation pipeline now unifies parameters from a forward time specified neutral island assembly model with a backwards time hierarchical population genetic model under the standard coalescent. Given the genetic data alone, a random-forest classifier and hierarchical approximate Bayesian computation have enabled estimating parameters of the assembly model as well as the time-dependent species abundance distributions. We plan to: (1) add phylogenetic data as a third axis of data; (2) expand to enable next generation SNP data and low coverage whole genome data; (3) expand to parameterize non-neutral processes such as niche-filtering and competition; and (4) allow for soft and hard selective sweeps associated with the population genomic data using the *discsim* coalescent simulator. Simulations have validated that our approach can yield estimates under a neutral model and a goal of this workshop will be to extend this approach for non-neutral model such as stochastic competitive assembly. While neutral and non-neutral models are two extremes that are well recognized to be part of a continuum between the relative contributions of stochastic and deterministic processes [1], the relative strength of deterministic competition could be parameterized by the shape parameter under a flexible gamma distribution of colonization rates over time. By using new theory to explicitly parameterize the expected spatial and temporal distributions of colonization/expansion and speciation across a region under different models of community assembly, an integration between particular ecological models and population genomic theory is possible, allowing inference on the history of a whole community as well as being able to test competing models of community assembly.

6.1 Data Management Plan

1. *Which dataset(s) does the project rely on?* We plan to use molecular data from each of the chronosequences we have identified and we have chosen workshop participants because they are either the owners of these data sets, or have access to them (see section 5 and biosketches).

2. *Time required for data integration.* Some of the data is already in place, while other data is actively being accrued. The timeline for these activities is outlined in 6 above.
3. *Fate of aggregated/integrated data* The data consist of organismal specimen collections (including vertebrates, arthropods, and plants), genetic and genomic sequence data, ecological measurements, geospatial layers, and subsequent analyses and archives of all data. All data produced during this research will be freely available to the public; we anticipate no sensitive or confidential data. Sequence data have been (or will be) deposited in the NCBI Genbank (<http://www.ncbi.nlm.nih.gov/genbank/>), with raw sequence reads deposited in the NCBI Sequence Read Archive (<http://www.ncbi.nlm.nih.gov/sra>). Meta-data associated with nucleic acid sequences conform to the MIMS or MIMARKS standards for metagenomes and marker genes respectively and will be *be made available via the iDiv data portal*. Meta-data concerning the environments sampled conform to the Environmental Ontology (EnvO) standards
4. *Use of central iDiv facilities.* None required

7 Budget

8 Appendix

References

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General Information

Please complete the table below containing the general information.	
number	2
Working group title	Biodiversity Dynamics – The Nexus Between Space & Time
Acronym	sEcoEvo
Keywords (up to 5 words/terms)	Macroecology, population genetics, chronosequence neutral theory, maximum entropy
Project summary (from proposal)	A central challenge in understanding the origins of biodiversity is that, while we can observe and test local ecological phenomena, we must usually infer the longer-term outcomes.
Name of 1st applicant (name and surname)	Rosemary Gillespie
Professional status (Professor, Assistant professor, Associate professor, Senior scientist (> 5 years), Post-Doc (<5 years), PhD-student, other)	Professor
Home institute(s) of 1st applicant	University of California Berkeley, USA
Homepage of 1st applicant	https://nature.berkeley.edu/evolab/
Email address of 1st applicant	gillespie@berkeley.edu
Name of 2nd applicant (if applicable)	Michael Hickerson
Professional status (Professor, Assistant professor, Associate professor, Senior scientist (> 5 years), Post-Doc (<5 years), PhD-student, other)	Associate professor
Home institute(s) of 2nd applicant	City University of New York
Homepage of 2nd applicant	https://hickerlab.wordpress.com/
Email address of 2nd applicant	mhickerson@gmail.com
enlarge this list if necessary	
Are you applying for a 2nd meeting? (yes/no)	Yes
Duration of meeting(s) in days (1st/2nd meeting – if relevant)	5
Proposed possible meeting dates (DD/MM/YYYY-DD/MM/YYYY; propose if possible more than one date -for all meetings you are applying for- in case of overlapping or competing dates with other projects; please check calendar pages of sDiv)	27/11/2017-1/12/17; 26/03/2018-30/03/2018
Total working group costs (incl. 2nd meeting if relevant; excl. working group Postdoc – if applicable; taken from proposal table 3, section 7)	31,170
Number of working group participants (tentative)	19
PhD students among participants (yes/no; How many?)	1
Female ratio of participants in %	30%
Are you applying for a working group Postdoc? (yes/no)	No
Postdoc duration in month	
Postdoc name (name and surname)	
Current (last) institute	
Homepage	
Email address	
Please specify in a brief paragraph how likely it is that the project can be successful if no postdoc is granted (see for alternative plan 6.3.).	
Who are/is the iDiv contact(s) among the participants? (name and surname)	Jonathan Chase

Participant list

List at least 10 confirmed tentative participants (including the applicants - max. 2), but preferably no more than 15.

Note that at least one iDiv member (see website) needs to be included (please highlight).

Working group title

Applicants (provide CV's via template)	Name, affiliation, contact address	Field of expertise reason for being a participant	Professional status Professor, Assistant professor, Associate professor, Senior scientist (> 5 years), Post-Doc (<5 years), PhD student, other
Confirmed participants ... (add a row per person)			
Rosemary Gillespie	University of California Berkeley, USA; gillespie@berkeley.edu	Community assembly over evolutionary time using geological ages of islands; data on Hawaiian & Pacific island arthropods	Professor
Michael Hickerson	City University of New York, USA; mhickerson@ccny.cuny.edu	Phylogeographic theory and population genetics using hierarchical multi-species models	Associate professor
Jonathan Chase	sDiv, Leipzig, Germany; jonathan.chase@idiv.de	Biodiversity synthesis, community ecology, meta-analysis, biodiversity scaling, food webs, metacommunity, theory	Professor
Luke Harmon	University of Idaho, USA; lukeh@uidaho.edu	Phylogenetics, comparative methods, eco-evolutionary dynamics, ecological neutral models, and macroevolution	Associate professor
Andrew Rominger	University of California Berkeley, USA; ajrominger@gmail.com	Ecological & evolutionary theory using principles from statistics & stochastic processes. Knowledge of Hawaiian biodiversity data	Postdoc
Brent Emerson	Inst Prod Nat Agrobiol, Canary Is; bemerson@ipna.csic.es	Evolution and community ecology, micro- & macroevolutionary processes; extensive data from Canaries, Azores, Mascarenes	Research scientist
Rampal S. Etienne	Groningen Inst Evol Life Sci, Netherlands; r.s.etienne@rug.nl	Theoretical and evolutionary community ecology	Professor
Catherine Graham	Swiss Federal Research Inst (WSL), Zurich, Switzerland; catherine.graham@wsl.ch	Biogeography, macroecology, and community ecology of hummingbirds; mechanisms influencing diversity patterns	Senior Researcher
Joaquin Hortal	Mus Nac Cien Nat (CSIC), Madrid, Spain; jhortal@mncn.csic.es	Island biogeography, macroecology, theoretical modelling & trait diversity; focus on Atlantic islands	Senior scientist
Petr Kiel	sDiv, Leipzig, Germany; pkeil@seznam.cz	Spatial scaling of static and dynamic properties of biodiversity, especially on ecological time scales.	Postdoc
Tiffany Knight	sDiv, Leipzig, Germany; tiffany.knight@idiv.de	Combine ecological & evolutionary factors to assess biodiversity over large spatial & temporal scale using Anolis lizards	Professor
Luke Mahler	University of Toronto, Canada; luke.mahler@utoronto.ca	Theoretical models in evolutionary ecology drawing from adaptive dynamics, quantitative genetics & interaction networks	Assistant professor
François Massol	CNRS, Montpellier, France; francois.massol@univ-lille1.fr	Combining genomic and ecological approaches to examine evolutionary processes	Researcher
Angela McLaughran	Australia National University; ang.mcgaughran@gmail.com	Large-scale ecology, ecoinformatics	Postdoc
Brian McGill	University of Maine, USA; mail@brianmcgill.org	Comparative phylogeography, population genetics, community assembly, modelling, Bioinformatics	Professor
Isaac Overcast	Graduate Center, City Univ New York; isaac.overcast@gmail.com	Using present-day patterns of biodiversity to infer past evolutionary processes; extensive data from Galapagos	PhD-student
Christine Parent	University of Idaho, USA; ceparent@uidaho.edu	Evolutionary adaptive radiation, influences on ecological communities, data on cichlid fish in African Rift lakes	Assistant professor
Catherine Wagner	University of Wyoming, USA; Catherine.Wagner@uwyo.edu		Assistant professor
Tentive participants ... (add a row per person)			
James Rosindell	Imperial College, London, England; j.rosindell@imperial.ac.uk	Ecological neutral theory, island biogeography, applying spatially explicit coalescence to maximise computational tractability	Research Fellow

Type of working group

Indicate whether this is a research, a strategic, or a outreach working group and, if applicable, how the characteristics of them might overlap.

Research working group

Budget calculation table				
Date		Meeting 1 (<DATES>)	Meeting 2 (<DATES>)	Meeting 3 (<DATES>)
No. of meeting days (5 days recommended)		5	5	
Travel expenses*				
Number of participants (EU)		5	4	
Travel expenses (EU) (average 300,- € p.p.)	300.00 €	1,500.00 €	1,200.00 €	- €
Number of participants (non-EU)		9	3	
Travel expenses (non-EU) (average of 1300,- € p.p.)	1,300.00 €	11,700.00 €	3,900.00 €	- €
Number of local participants (from Leipzig)		3	3	
Total travel expenses		13,200.00 €	5,100.00 €	- €
Daily expenses				
Total hotel expenses (external participant/day 70,- €)	70.00 €	5,880.00 €	2,940.00 €	- €
Total daily (food) expenses (p.p./day 30,- €)	30.00 €	2,550.00 €	1,500.00 €	- €
TOTAL expenses per meeting (costs for postdoc not included)		21,630.00 €	9,540.00 €	- €
Postdoc (if proposed)				
Duration of postdoc's stay in Leipzig (in months)				
Additional costs for Postdoc (Please be as specific as possible):				
Travel costs				
Publication costs				
Other (Please specify)				
* based on average expenses of past sDiv working groups. If you expect your travel expenses to differ from our calculation please specify here (e.g. in case of many regional participants):				

Type of application: workshop participant

Name: Rosemary G Gillespie
 Nationality: British
 Address: 130 Mulford Hall, University of California Berkeley, CA 94720-3114
 E-mail: gillespie@berkeley.edu
 URL: <http://nature.berkeley.edu/~gillespie/> & <http://nature.berkeley.edu/evolab>
 Professional status: Professor

Education

1980	Edinburgh University, Zoology, Biology, BSc. Hons.
1986	University of Tennessee, Zoology, Ph.D.

Academic positions

1999-2002	Schlinger Chair in Systematics and Professor, Dept. Env. Science, Policy & Management, University of California, Berkeley
1999-2013	Director, Essig Museum of Entomology, University of California, Berkeley Chair, Berkeley Natural History Museums (Museum Vertebrate Zoology, UC Museum of Paleontology, UC & Jepson Herbaria, Essig Museum of Entomology, Botanical Garden, Hearst Museum of Anthropology)
2004-2012	Chair, Ecol, Evol & Conservation Biol Grad Program, Univ. Hawaii. Associate Professor of Zoology and Associate Researcher, Center for Conservation Research & Training, PBRC, Univ. Hawaii.
1994-1998	Chair, Ecol, Evol & Conservation Biol Grad Program, Univ. Hawaii.
1992-2000	Associate Professor of Zoology and Associate Researcher, Center for Conservation Research & Training, PBRC, Univ. Hawaii.
2008-present	Assoc Editor, <i>Molecular Ecology</i> 2008-2016; Senior Editor 2016-present
2008-present	Trustee & Fellow, California Academy of Sciences
2016-present	Associate Editor, <i>Journal of Biogeography</i>
2008-2011	President, <i>American Arachnological Society</i>
2013-2015	President, <i>International Biogeography Society</i> (Past Pres 2015-2017)
2016 – present	President elect, <i>American Genetics Association</i>

General expertise Research has focused on community assembly over ecological and evolutionary time, using geological chronosequences provided by island archipelagoes. We examine adaptive radiations across multiple islands, with particular emphasis on arthropods in the Hawaiian Islands. Using the island chronosequence, our research integrates macroecological and microevolutionary approaches to provide insights into the temporal dynamics of diversification.

Five important & relevant publications (h-index=40; i10-index= 108; 3885 citations/ 2012)

- Shaw, K.L. and Gillespie, R.G. 2016. Comparative phylogeography of oceanic archipelagos: Hotspots for inferences of evolutionary process. *Proceedings of the National Academy of Sciences* 113(29): 7986-7993
- Gillespie, R.G. 2016. Island time and the interplay between ecology & evolution in species diversification. *Evolutionary Applications*. 9(1), pp.53-73.
- Rominger, A.J., Goodman, K. R., Lim, J.Y., Valdovinos, F.S., Armstrong, E., Bennett, G. M., Brewer, M. S., Cotoras, D. D., Ewing, C. P., Harte, J., Martinez, N., O'Grady, P., Percy, D., Price, D., Roderick, G. K., Shaw, K., Gruner, D. S., Gillespie, R. G. 2016. Community assembly on isolated islands: Macroecology meets evolution. *Global Ecology and Biogeography* 25, 769-780.
- Emerson, B.C. and R.G. Gillespie. 2008. Phylogenetic analysis of community assembly and structure over space and time. *Trends in Ecology & Evolution* 23(11): 619-630.
- Gillespie, R. G. 2004. Community assembly through adaptive radiation in Hawaiian spiders. *Science* 303 (5656): 356-359

Type of application: workshop participant

Name:	Michael J. Hickerson
Nationality:	United States
Address:	City College of New York Biology Department 160 Convent Ave New York, NY 10031
	Fax: 212-650-8585
	E-mail: mhickerson@ccny.cuny.edu
	URL: http://hickerlab.wordpress.com/
Professional status:	Associate professor

Education

B.S. 1990-1993	The Evergreen State College
M.S. 1996-1997	Western Washington University
Ph.D. 1998-2003	Duke University

Academic positions

2014 – present	Associate professor, City College (CUNY), New York, NY
2012 – 2014	Assistant professor, City College (CUNY), New York, NY
2007 – 2012	Assistant professor, Queens College (CUNY), Flushing, NY
2007 – present	Affiliated professor, CUNY Graduate sub-program in Evolution, Ecology and Behavior, New York, NY

General expertise

Comparative phylogeography and population genetics using hierarchical multi-species models

Five important & for the project relevant publications (h-index= 25; i10-index 36)

- Alvarado-Serrano, D.F. & Hickerson, M.J., 2015. Spatially explicit summary statistics for historical population genetic inference. Methods in ecology and evolution / British Ecological Society. Available at: <http://onlinelibrary.wiley.com/doi/10.1111/2041-210X.12489/full>.
- Burbrink, F.T. et al., 2016. Asynchronous demographic responses to Pleistocene climate change in Eastern Nearctic vertebrates. Ecology letters. Available at: <http://onlinelibrary.wiley.com/doi/10.1111/ele.12695/full>.
- Prates, I. et al., 2016. Inferring responses to climate dynamics from historical demography in neotropical forest lizards. Proceedings of the National Academy of Sciences, 113(29), pp.7978–7985.
- Smith, B.T. et al., 2014. The drivers of tropical speciation. Nature, 515(7527), pp.406–409.
- Xue, A.T. & Hickerson, M.J., 2015. The aggregate site frequency spectrum (aSFS) for comparative population genomic inference. Molecular ecology. Available at: <http://dx.doi.org/10.1111/mec.13447>
-

Appendix I: Template for CVs

Type of application: *Working group applicant/participant*

Name: Jonathan Chase
Nationality: United States (residing in Germany)
Address: German Centre for Integrative Biodiversity Research (iDiv)
Deutscher Platz 5e
Leipzig, Germany
E-mail: jonathan.chase@idiv.de

Professional status: Professor

Education

1998 PhD. Department of Ecology and Evolution, University of Chicago
1995 M.S. Department of Fisheries and Wildlife, Utah State University
1992 B.S. School of Natural Resources, University of Michigan

Academic Positions

2014-Present Professor of Biodiversity Synthesis, iDiv
Professor, Department of Computer Science, MLU Halle

2012-2014 Senior Scientist, Biodiversity Synthesis Lab, Saint Louis

2002-2011 Assist, Assoc, and Full Professor, Washington University in Saint Louis

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General expertise

Biodiversity synthesis, community ecology, meta-analysis, biodiversity scaling, food webs, metacommunity, theory, experiments

Five important publications

Leibold, M.A. and J. M. Chase 2017. Metacommunity ecology. Princeton University Press.
Chase, J. M. and T. M. Knight. 2013. The scale-dependent influence of global change on patterns of biodiversity. *Ecology Letters* 16: 17-26.
Powell, K. I., J. M. Chase and T. M. Knight. 2013. Invasive plants have scale-dependent effects on biodiversity by altering the species-area relationship. *Science* 339: 316-318
Chase, J. M. and J. A. Myers. 2011. Disentangling the importance of ecological niches from stochastic processes across scales. *Philosophical Transactions of the Royal Society of London (B)* 366: 2351-2363
Chase, J.M. 2010. Stochastic community assembly causes higher biodiversity in more productive environments. *Science* 328: 1388-1391.

Type of application: working group participant

Name: Luke J. Harmon
Nationality: USA
Address: University of Idaho
875 Perimeter Drive MS 3051
Moscow, ID USA 83844-3051
Fax: 208-885-7905
E-mail: lukeh@uidaho.edu
URL: <http://lukejharmon.github.io/>
Professional status: Associate professor

Education

2005	Washington University, St. Louis, MO Ph. D. in Evolution, Ecology, and Population Biology
1998	Iowa State University, Ames, IA B.S. with honors, summa cum laude Major: Zoology Minor: Mathematics

Academic positions

2012-present	Associate Professor, Dept. of Biological Sciences University of Idaho
2007-2012	Assistant Professor, Dept. of Biological Sciences University of Idaho
2005-2007	Postdoctoral Fellow, Biodiversity Research Centre University of British Columbia, Vancouver, B.C. Supervisor: Dr. Dolph Schlüter

General expertise (and its relevance for the working group if application is attached on working group)

My expertise is in phylogenetics, comparative methods, eco-evolutionary dynamics, ecological neutral models, and macroevolution. All of these topics relate closely to the focus of the working group.

Five important & for the project relevant publications (h-index= 38, 5316 total citations since 2012)

- Rosindell, J., **L. J. Harmon**, and R. S. Etienne. 2015. Unifying ecology and macroevolution with individual-based theory. *Ecology Letters* 18: 472-482.
- Nuismer, S. L. and **L. J. Harmon**. 2015. Predicting rates of interspecific interaction from phylogenetic trees. *Ecology Letters* 18: 17-28.
- Uyeda, J. C. and **L. J. Harmon**. 2014. A novel Bayesian method for inferring and interpreting the dynamics of adaptive landscapes from phylogenetic comparative data. *Systematic Biology* 63: 902-918.
- Pennell, M. W., J. M. Eastman, G. J. Slater, J. W. Brown, J. C. Uyeda, R. G. Fitzjohn, M. E. Alfaro, and **L. J. Harmon**. 2014. geiger v2.0: an expanded suite of methods for fitting macroevolutionary models to phylogenetic trees. *Bioinformatics* 30: 2216-2218.
- Harmon, L. J.**, J. A. Schulte, J. B. Losos, and A. Larson. 2003. Tempo and mode of evolutionary radiation in iguanian lizards. *Science* 301: 961-964.
-

Type of application: working group applicant

Name: Andrew J. Rominger
Nationality: USA
Address: Department of Environmental Science, Policy & Management
University of California, Berkeley 130 Mulford Hall
Berkeley, CA 94720 USA

E-mail: rominger@berkeley.edu
URL: nature.berkeley.edu/~rominger
Professional status: Post-Doc (<5 years)

Education

2009 B.S. in Biological Sciences, Stanford University
2016 Ph.D. in Environmental Science, Policy and Management, University of California, Berkeley

Academic positions

2017 Postdoctoral Scholar, Berkeley Initiative in Global Change Biology, UC Berkeley

General expertise (and its relevance for the working group if application is attached on working group)

Developing and testing ecological and evolutionary theory using principles from statistical physics and stochastic processes. Developing and implementing best statistical practices for ecological and genetic data, including proficiency in developing and optimizing Bayesian hierarchical models. Detailed knowledge of biodiversity across the Hawaiian Islands.

Five important & for the project relevant publications (h-index= 5, 157 citations/2017)

Rominger AJ & Merow C (2016) meter: an R package for testing the maximum entropy theory of ecology. **Methods in Ecology and Evolution**.

Rominger AJ, Goodman K, Lim J, et al. (2015) Community assembly on isolated islands: macroecology meets evolution. **Global Ecology and Biogeography**.

Harte J, **Rominger AJ** & Zhang W (2015) Integrating macroecological metrics and community taxonomic structure. **Ecology Letters** 18: 1068–1077.

Karp DS, **Rominger AJ**, Zook J, Ranganathan J, Ehrlich PR & Daily GC (2012) Intensive agriculture erodes β-diversity at large scales. **Ecology Letters** 15: 963–970

Rominger AJ, Miller TE & Collins SL (2009) Relative contributions of neutral and niche-based processes to the structure of a desert grassland grasshopper community. **Oecologia** 161: 791–800

Template for CVs

Type of application: working group participant

Name: Brent Charles Emerson
Nationality: New Zealand / British
Address: Island Ecology and Evolution Research Group, IPNA-CSIC, C/ Astrofísico Francisco Sánchez 3, La Laguna, Santa Cruz de Tenerife - Spain
E-mail: bemerson@ipna.csic.es
URL: www.brentemerson.com
Professional status: Research Scientist

Education

1987-1990 B.Sc. Hons. First Class (University of Otago, New Zealand)
1991-1994 Ph.D. (University of Otago, New Zealand)

Academic positions

2011- Research Scientist, Spanish National Research Council, Spain
2001-2011 Lecturer, Senior Lecturer, then Reader in Evolutionary Biology, University of East Anglia, UK

General expertise Dr Emerson is a leading international researcher in the fields of evolution and community ecology, who has produced significant theoretical and empirical contributions to our knowledge of the micro- and macroevolutionary processes involved in speciation, with a strong emphasis on insular environments and invertebrates. Dr. Emerson was made a Fellow of the Linnean Society (UK) in 2007 in recognition of his contributions in evolution and ecology, and received a Leverhulme Trust research fellowship in 2009. With 112 articles in peer-reviewed journals, many of them in high-impact journals (e.g. Nature, Science), Emerson's work has had a high impact on the scientific community (> 4800 citations). His most recent work (i) developing NGS tools for biodiversity analysis and (ii) developing and implementing community-scale biodiversity sampling programs, clearly aligns his research with the objectives of the working group.

Five important & for the project relevant publications

- Cicconardi, F., P. A. V. Borges, D. Strasberg, P. Oromí, H. López, A. J. Pérez-Delgado, J. Casquet, J. Caujapé-Castells, J. M. Fernández-Palacios, C. Thébaud & **B. C. Emerson** (2017). MtDNA metagenomics reveals large-scale invasion of belowground arthropod communities by introduced species. **Molecular Ecology**, in press.
- Patiño, J., R. Whittaker, P. A. V. Borges, J. M. Fernández-Palacios, C. Ah-Peng, M. Araujo, S. Ávila, P. Cardoso, J. Cornuault, E. J. de Boer, L. de Nascimiento, A. Gil, A. González-Castro, D. S. Gruner, R. Heleno, J. Hortal, J. C. Illera, C. Kaiser-Bunbury, T. Matthews, A. Papadopoulos, N. Pettorelli, J. Price, A. M. C. Santos, M. J. Steinbauer, K. A. Triantis, L. Valente, P. Vargas, P. Weigelt & **B. C. Emerson** (2017). A roadmap for island biology: 50 fundamental questions after 50 years of *The Theory of Island Biogeography*. **Journal of Biogeography**, in press.
- Emerson, B. C.**, J. Casquet, H. López, P. Cardoso, P. A. V. Borges, N. Mollaret, P. Oromí, D. Strasberg & C. Thebaud. (2017). A combined field survey and molecular identification protocol for comparing forest arthropod biodiversity across spatial scales. **Molecular Ecology Resources**, in press.
- Emerson, B. C.** & R. G. Gillespie (2008) Phylogenetic approaches to community assembly and structure over space and time. **Trends in Ecology and Evolution**, 23:619-630.
- Emerson, B. C.**, & N. Kolm. (2005). Species diversity can drive speciation. **Nature**, 434:1015-1017.
-

Type of application: workshop participant

Name: Rampal S. Etienne
Nationality: The Netherlands
Address: University of Groningen, Box 11103, 9700 CC Groningen, The Netherlands
Fax: -
E-mail: r.s.etienne@rug.nl
URL: <http://www.rug.nl/staff/r.s.etienne/>
Professional status: Associate professor

Education

1996 MSc. Physics @ Utrecht University, The Netherlands
1997 MSc. Environmental Science @ University of Nijmegen, The Netherlands
1999 MSc. Philosophy of Science @ Utrecht University, The Netherlands
2002 PhD. Metapopulation biology @ Wageningen University, The Netherlands

Academic positions

1997-1998 Lecturer Environmental Modelling
1998-2002 PhD student, Wageningen University, The Netherlands
2002 Postdoc, Wageningen University, The Netherlands
2002-2004 Postdoc, University of Groningen, The Netherlands
2004-2007 Postdoc, University of Groningen, The Netherlands
2008-2012 Assistant professor, University of Groningen, The Netherlands
2012-present Associate professor, University of Groningen, The Netherlands

General expertise (and its relevance for the working group/workshop if application is attached on workshop/working group)

Theoretical and Evolutionary Community Ecology

Five important & for the project relevant publications (h-index=31,62 citations/31-01-2017)

- Van Velzen, E., S. Perez-Vila & **R.S. Etienne** (2016). The role of within-host competition for coexistence in multiparasitoid-host systems. *American Naturalist* 187: 48-59.
- Valente, L.M., Phillimore A.B. & **Etienne, R.S.** (2015). Equilibrium and non-equilibrium dynamics simultaneously operate in the Galápagos islands. *Ecology Letters* 18: 844-852.
- Pigot, A.L. & **Etienne, R.S.** (2015). A new dynamic null model for phylogenetic community structure. *Ecology Letters* 18: 153-163.
- Van Velzen, E. & **R.S. Etienne**. (2015). The importance of ecological costs for the evolution of plant defense against herbivory. *Journal of Theoretical Biology* 372: 89-99.
- Etienne, R.S.**, Haegeman, B. (2012) A conceptual and statistical framework for adaptive radiations with a key role for diversity-dependence. *American Naturalist* 180: E75-E89
-

Type of application: Working group participant

Name: Catherine Graham
Nationality: American
Address: Swiss Federal Research Institute (WSL);
Zürcherstrasse 111; CH-8903, Birmensdorf
Fax: +41 44-739 22 15
E-mail: catherine.graham@wsl.ch
URL: <http://catherinegraham.weebly.com>
Professional status: Senior Scientist (WSL) / Full Professor (Stony Brook University)
>5yrs

Education

1992 BA, Eckerd College, St. Petersburg, Florida
1995 MA, University of Missouri - St. Louis, Missouri
2000 PhD, University of Missouri - St. Louis, Missouri

Academic positions

2003-2016 Assistant to Full Professor, Dept. of Ecol.& Evol., Stony Brook University
2009-2015 Senior Researcher, Swiss Federal Research Institute (WSL)

General expertise

Biogeography, macroecology, and community ecology of hummingbirds; mechanisms influencing diversity patterns from local to global scales; beta-diversity

Five important & for the project relevant publications (h-index= 44, 19,000 citations/Feb 2017; based on google scholar)

- Machac, A. and **C.H. Graham**. *In press*. Geographically uneven expansion of mammalian diversity. *American Naturalist*.
- Fritz, S.A., J.T. Eronen, J. Schnitzler, C.H. Hof, C.M. Janis, A. Mulch, K. Böhning-Gaese, **C.H. Graham**. *Early view*. Twenty-million-year relationship between mammalian diversity and primary productivity. *Proceedings of the National Academy of Sciences*.
- Graham, C.H.**, A.C. Carnaval, T. E. Roberts, C.D. Cadena, C.M. McCain, R. C.K. Bowie, C. Moritz, J.L. Parra, C.J. Schneider, J. VanDerWal, K.R. Zamudio, C. Rahbek K.H. Kozak and N.J. Sanders. *2014*. The origin and maintenance of montane biodiversity: integrating evolutionary and ecological processes. *Ecography*, 37: 1-9.
- Graham, C.H.** and P. Fine (authors contributed equally). *2008*. Phylogenetic beta diversity: Linking ecological and evolutionary processes across space and time. *Ecology Letters* 11: 1265-1277.
- Graham, C.H.**, C. Moritz and S.E. Williams. *2006*. Habitat history improves prediction of biodiversity in a rainforest fauna. *Proceedings of the National Academy of Sciences*, 103: 632-636.

Type of application: working group participant

Name: Joaquín Hortal
Nationality: Spanish
Address: Departamento de Biogeografía y Cambio Global
Museo Nacional de Ciencias Naturales (CSIC)
C/José Gutiérrez Abascal 2, 28006 Madrid, Spain
Tel: +34 914111328 ext. 1284 Fax: +34915645078
E-mail: jhortal@mncn.csic.es; jqhortal@gmail.com
URL: <http://jhortal.com/>

Professional status: Senior scientist (>5 years)

Education

1999–2004 PhD Evolutionary Biology and Biodiversity, Univ Autónoma Madrid, Spain
2000–2002 MSc Evolutionary Biology and Biodiversity, Univ Autónoma Madrid, Spain
1996–1997 MSc Education and Pedagogy, Univ Complutense Madrid, Spain
1990–1996 BSc Biology, Environmental Biology, Univ Autónoma Madrid, Spain

Academic positions

2016- Tenured Scientist, Museo Nacional Ciencias Naturales (CSIC), Spain
2010- Visiting Professor, Dept. Ecología, Universidade Federal de Goiás, Brazil
2010-2016 RyC Research Fellow, Museo Nacional Ciencias Naturales (CSIC), Spain
2007-2010 Research associate, NERC CPB, Imperial College London, UK
2005-2007 Postdoctoral researcher, Center for Macroecology, Univ Copenhagen, Denmark & Azorean Biodiversity Group, Univ Açores, Portugal
1999-2004 PhD Student, Museo Nacional de Ciencias Naturales (CSIC), Spain

General expertise (and its relevance for the working group if application is attached on working group)

Research topics: Biogeography, Biodiversity, Macroecology, Community Ecology, Conservation, Entomology
Areas of expertise: Island Biogeography, Theoretical modelling, Trait diversity, Functional ecology, Biodiversity measurement, Biodiversity databases

Five important & for the project relevant publications (h-index= 29, 3028 citations/17 January 2017)

- Borges, P.A.V.* & **Hortal, J.*** (2009) Time, area and isolation: Factors driving arthropod speciation at the Azorean Archipelago. *Journal of Biogeography*, 36, 178–191. doi:10.1111/j.1365-2699.2008.01980.x [*** shared 1st authorship**]
- Hortal, J.**, Triantis, K.A., Meiri, S., Thébaud, E., & Sfenthourakis, S. (2009) Island species richness increases with habitat diversity. *American Naturalist*, 173, E205–E217. doi:10.1086/645085
- Hortal J.**, Diniz-Filho J.A.F., Bini L.M., Rodríguez M.Á., Baselga A., Nogués-Bravo D., Rangel T.F., Hawkins B.A. & Lobo J.M. (2011) Ice age climate, evolutionary constraints and diversity patterns of European dung beetles. *Ecology Letters*, 14, 741–748. doi:10.1111/j.1461-0248.2011.01634.x
- Gouveia, S.F., **Hortal, J.**, Tejedo, M., Duarte, H., Cassemiro, F.A.S., Navas, C.A. & Diniz-Filho, J.A.F. (2014) Climatic niche at physiological and macroecological scales: the thermal tolerance–geographical range interface and niche dimensionality. *Global Ecology and Biogeography*, 23, 446–456. doi:10.1111/geb.12114
- Calatayud, J., Hórreo, J.L., Madrigal-González, J., Migeon, A., Rodríguez, M.Á., Magalhães, S. & **Hortal, J.** (2016) Geography and major host evolutionary transitions shape the resource use of plant parasites. *Proceedings of the National Academy of Sciences USA*, 113, 9840–9845. doi:10.1073/pnas.1608381113
-

Template for CVs

Type of application: Working group participant.

Name: Petr Keil
Nationality: Czech Republic
Address: iDiv, Deutscher Platz 5e, 04103 Leipzig, Germany

E-mail: petr.keil@idiv.de
URL: www.petrkeil.com

Professional status: Postdoc

Education

2006-2010 PhD, Department of Ecology, Charles University in Prague, Czech Rep.
2000-2005 B.Sc. and M.Sc. in zoology. University of South Bohemia. Czech Rep.

Academic positions

2015-present Postdoc, iDiv, Leipzig, Germany
2011-2014 Postdoc, Yale University, USA
2011, 2012-2012 Postdoc, Charles University in Prague, Czech Rep.

General expertise (and its relevance for the working group if application is attached on working group)

PK's main expertise is in spatial scaling of both static and dynamic properties of biodiversity, especially on ecological time scales. He published on species-area, endemics-area and on scaling of temporal biodiversity change and beta diversity; he also designed hierarchical statistical models of biodiversity and its temporal dynamics. Second, PK has recently developed a model estimating evolution of species ranges from contemporary range data. Third, PK has an expertise in simulation modelling, specifically in neutral models of biodiversity and in models of species geographic range placement. Finally, PK has a strong background in likelihood-based and Bayesian statistics, which will be priceless in the empirical parts of the project.

Five important & for the project relevant publications (h-index=15, 713 citations/Feb 9 2017, Google Scholar)

Quintero I, **Keil P**, Jetz W & Crawford FW (2015) Historical biogeography using species geographic ranges. **Systematic Biology** 64: 1059-1073.

Keil P, Belmaker J, Wilson AM, Unitt P & Jetz W (2013) Downscaling of species distribution models: a hierarchical approach. **Methods in Ecology and Evolution** 4: 82-94.

Keil P et al. (2012) Patterns of beta diversity in Europe: the role of climate, land cover and distance across scales. **Journal of Biogeography**, 39: 1473-1486.

Storch D, **Keil P** & Jetz W (2012) Universal species-area and endemics-area relationships at continental scales. **Nature**, 488: 78-81.

Keil P, Herben T, Rosindell J & Storch D (2011) Predictions of Taylor's power law, density dependence and pink noise from a neutrally modelled time series. **Journal of Theoretical Biology** 265: 78-86.

Tiffany M. Knight

Name:	Prof. Knight, Tiffany Marie
Nationality:	US American
Address:	German Center for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Deutscher Platz 5e, 04103 Leipzig, Germany
E-mail:	Tiffany.Knight@idiv.de
URL:	http://bit.ly/2dhpKG1
Professional status:	Alexander von Humboldt Professorship and Head of Research Group <i>Spatial Interaction Ecology</i> - Martin Luther University Halle- Wittenberg, Helmholtz Centre for Environmental Research- UFZ, German Center for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Education

1997-2003	University of Pittsburgh, PhD in Ecology and Evolution
1993-1997	Florida State University, B.S. in Biology

Academic positions

2016-present	Alexander von Humboldt Professorship and Head of Research Group <i>Spatial Interaction Ecology</i>
2014-2015	Visiting Scientist (while on academic sabbatical), German Center for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
2010-2015	Associate Professor (with tenure), Department of Biology, Washington University in St. Louis
2012-2013	Visiting Scientist (while on academic sabbatical), Department of Botany, University of Hawaii
2010-2014	Director, Environmental Studies Program, Washington University in St. Louis
2005-2010	Assistant Professor, Department of Biology, Washington University in St. Louis
2006-present	Research Associate, Chicago Botanic Garden
2005-present	Research Associate, Missouri Botanical Garden
2004-2005	Postdoctoral Research Associate, National Center for Ecological Analysis and Synthesis, Santa Barbara, California
2003-2004	Postdoctoral Research Associate, Department of Zoology, University of Florida

General expertise

Empirical experience in plant ecology assessing how environmental drivers affect the diversity and composition of plant communities.

Five important publications (Overall h-index= 35, Total number of citations: 5129, Web of Science/14 February 2017)

- Bernardo, H. L., Albrecht, M. A., & **Knight, T. M.** (2016). Increased drought frequency alters the optimal management strategy of an endangered plant. *Biological Conservation*, 203, 243-251.
- Burkle, L.A., Marlin, J.C. and **Knight, T.M.** (2013). Plant-Pollinator Interactions over 120 Years: Loss of Species, Co-Occurrence and Function. *Science* 339: 1611-1615.
- Powell, K.I., Chase, J.M. and **Knight, T.M.** (2013). Invasive plants have scale-dependent effects on biodiversity by altering the species-area relationship. *Science* 339: 316-318.
- Dangremond, E.M., Pardini, E.A. and **Knight, T.M.** (2010). Apparent competition with an invasive plant hastens the extinction of an endangered lupine. *Ecology* 91: 2261-2271.
- Knight, T.M.**, McCoy, M.W., Chase, J.M., McCoy, K.A. and Holt, R.D. (2005): Trophic cascades across ecosystems. *Nature* 437: 880-883

Type of application: working group participant

Name: D. Luke Mahler
Nationality: USA (but permanent resident of Canada)
Address: 404 Huron St., Apt. 2
Toronto, Ontario M5S 2G6
Canada
Fax: 416-978-5878
E-mail: luke.mahler@utoronto.ca
URL: <https://mahlerlab.com>
Professional status: Assistant professor

Education

2011 Ph.D., Organismic and Evolutionary Biology, Harvard University
2003 B.A., Biology with Honors, University of Chicago

Academic positions

2015 Assistant Professor, Dept. of Ecology & Evolutionary Biology, University of Toronto
2014 Postdoctoral Fellow, Dept. of Ecology & Evolutionary Biology, University of Kansas
2011 Center for Population Biology Postdoctoral Fellow, UC Davis

General expertise (and its relevance for the working group if application is attached on working group)

I aim to understand how ecological and evolutionary factors combine to generate biodiversity over large spatial and temporal scales. To do this, I conduct research on a natural macroevolutionary experiment: repeated adaptive radiations of neotropical *Anolis* lizards (i.e., “anolies”). These lizards provide a unique system for studying the role of ecology in macroevolution because they have diversified repeatedly in both similar and different ecological settings throughout the New World tropics. With recent NSERC-funded work, my lab is investigating whether greater functional richness on larger islands stems from enhanced alpha or beta diversity.

Five important & for the project relevant publications (h-index= 16, 1321 citations/Feb. 9, 2017)

- Mahler, D. L., S. M. Lambert, A. J. Geneva, J. Ng, S. B. Hedges, J. B. Losos, and R. E. Glor. 2016. Discovery of a giant chameleon-like lizard (*Anolis*) on Hispaniola and its significance to understanding replicated adaptive radiations. *The American Naturalist* 188:357-364.**
- Algar, A. C., and D. L. Mahler. 2015. Area, climate heterogeneity, and the response of climate niches to ecological opportunity in island radiations of *Anolis* lizards. *Global Ecology and Biogeography*. DOI: 10.1111/geb.12327**
- Sherratt, E., M. del R. Castañeda, M. Garwood, D. L. Mahler, T. J. Sanger, A. Herrel, K. de Queiroz, J. B. Losos. 2015. Amber fossils demonstrate deep-time stability of Caribbean lizard communities. *PNAS* 112:9961-9966.**
- Helmus, M. R., D. L. Mahler, and J. B. Losos. 2014. Island biogeography in the Anthropocene. *Nature* 513:543-546.**
- Mahler, D. L., T. Ingram, L. J. Revell, and J. B. Losos. 2013. Exceptional convergence on the macroevolutionary landscape in island lizard radiations. *Science* 341:292-295.**
-

Type of application: working group participant

Name: **François Massol**
Nationality: French
Address: Evo-Eco-Paleo unit (UMR 8198 CNRS / Univ. Lille), Bat SN2, University of Lille Science & Technology campus, F-59655 Villeneuve d'Ascq cedex, France
E-mail: francois.massol@univ-lille1.fr Fax: +33320436979
URL: <https://sites.google.com/a/polytechnique.org/francoismassol/home>
Professional status: Permanent researcher at the CNRS (since 2012)

Education

2015 Habilitation in Biodiversity Science, University of Lille, France
2008 PhD in Population Biology & Ecology, University of Montpellier, France
2004 MSc in Evolutionary Biology & Ecology, University of Montpellier, France
2003 MSc, ENGREF, Paris, France
2002 MSc, Ecole Polytechnique, Palaiseau, France

Academic positions

2013 - Permanent researcher at the CNRS, Lille, France
2012 - 2014 Permanent researcher at the CNRS, Montpellier, France
2009 - 2010 Post-doctoral fellow at the University of Texas, Austin, USA
2008 - 2012 Permanent researcher IRSTEA, Aix-en-Provence, France

General expertise

Formalization and analysis of theoretical models in evolutionary ecology, mainly drawing from adaptive dynamics, quantitative genetics and the evolutionary ecology of interaction networks
Development of methods for the analysis of ecological datasets, with a focus on metacommunities and ecological networks
Life-history trait evolution and invasion biology, especially regarding the causes and consequences of dispersal syndromes for plant-pollinator interactions and the properties of food webs

Five important & for the project relevant publications (h-index= 15, 697 citations/ Feb. 7th 2017)

Astegiano, J., Guimarães, P. R. Jr., Cheptou, P.-O., Vidal-Morais, M. M., Mandai, C. Y., Ashworth, L., & **Massol, F.** (2015) Persistence of plants and pollinators in the face of habitat loss: Insights from trait-based metacommunity models. *Advances in Ecological Research*, **53**, 201-257.

Calcagno, V.*, **Massol, F.***, Mouquet, N., Jarne, P., & David, P. (2011) Constraints on food chain length arising from regional metacommunity dynamics. *Proceedings of the Royal Society Biological Sciences Series B*, **278**, 3042-3049.

Duputié, A., **Massol, F.**, Chuine, I., Kirkpatrick, M., & Ronce, O. (2012) How do genetic correlations affect species range shifts in a changing climate? *Ecology Letters*, **15**, 251-259.

Gravel, D.*, **Massol, F.***, & Leibold, M. (2016) Stability and complexity in model meta-ecosystems. *Nature Communications*, **7**, 12457.

Laroche, F., Jarne, P., Lamy, T., David, P., & **Massol, F.** (2015) A neutral theory for interpreting correlations between species and genetic diversity in communities. *American Naturalist*, **185**, 59-69.

* indicates co-first authorship

Type of application: working group applicant

Name:	Angela McGaughran
Nationality:	New Zealand
Address:	Australian National University; Research School of Biology; Evolution, Ecology and Genetics; Canberra ACT 2601; Australia
	E-mail: ang.mcgaughran@gmail.com
URL:	https://scholar.google.com.au/citations?hl=en&user=ahigy_4AAAAJ&view_op=list_works
Professional status:	Post-Doc (>5 years)

Education

2006-2009:	PhD (Molecular BioSciences); Massey University, Palmerston North, New Zealand
2003-2005:	MSc (Genetics), first class honours; Waikato University, Hamilton, New Zealand
2000-2002:	BSc (Biology); Waikato University, Hamilton, New Zealand

Academic positions

2016 - ongoing	Post-Doctoral Fellowship (Historical population genomics); Australian National University, Canberra, Australia
2014-2015:	Post-Doctoral Fellowship (Comparative population genomics); Commonwealth Scientific Industrial and Research Organisation (CSIRO), Canberra, Australia
2010-2014:	Post-Doctoral Fellowship (Population genomics); Max Planck Institute for Developmental Biology, Tuebingen, Germany

General expertise (and its relevance for the working group)

My expertise is in the field of population genomics and I have a strong documented record investigating the patterns and processes relating to species distributions and their population genetic structure/s. My recent work attests to my interest in integrating a population genomics focus into biogeographic and macroecological research, namely by tying together landscape-level processes across species into a cohesive framework that identifies broad-scale patterns.

Five important & for the project relevant publications (h-index= 12, 13/02/17)

1. McGaughran A (2015) Integrating a population genomics focus into biogeographic and macroecological research. **Frontiers in Ecology and Evolution: Biogeography and Macroecology** 3:132-136. (0 citations)

2. McGaughran A, Rödelsperger C, Grimm D, Meyer JM, Moreno E, Morgan K, Leaver M, Serobyan V, Rakitsch B, Borgwardt KM, Sommer RJ (2016) Genome-wide profiles of diversification and genotype-phenotype association in nematodes from La Réunion Island. **Molecular Biology and Evolution** 33:2257-2272. (4 citations)

3. Fraser C, McGaughran A, Chuah A, Waters J (2016) The importance of replicating genomic analyses to verify phylogenetic signal for recently evolved lineages. **Molecular Ecology** 25:3683-3695. (1 citation)

4. Sommer RJ, McGaughran A (2013) The nematode *Pristionchus pacificus* as a model system for integrative studies in evolutionary biology. **Molecular Ecology** 22:2380-2393. (38 citations)

5. McGaughran A, Stevens MI, Hogg ID, Carapelli A (2011) Extreme glacial legacies: a synthesis of the Antarctic springtail phylogeographic record. **Insects** 2:62-82. (20 citations)

Template for CVs

Type of application: *working group participant*

Name: Brian McGill
Nationality: USA
Address: University of Maine; Orono, ME 04469; USA
Fax: (207) 581-2969
E-mail: mail@brianmcgill.org
URL: <http://www.brianmcgill.org>
Professional status: Professor

Education

2003	PhD in Ecology and Evolutionary Biology, University of Arizona
1988	BA in Mathematics, Harvard University

Academic positions

2010-present	University of Maine (Assistant Professor, Associate Professor, Professor)
2008-2010	University of Arizona (Assistant Professor)
2005-2008	McGill University (Assistant Professor)
2003-2005	NSF Bioinformatics Postdoctoral Fellow, Michigan State University

General expertise (and its relevance for the working group if application is attached on working group)

Large-scale ecology
Ecoinformatics

Five important & for the project relevant publications (h-index= 33, 6960 total citations, 4993 citations since 2012 all per Google Scholar as of Feb 10, 2017)

1. **McGill, Brian J**; Hadly, Elizabeth A; Maurer, Brian A "Community inertia of Quaternary small mammal assemblages in North America" (**Proceedings of the National Academy of Science** 2005 102:16701-16706) (94 citations)
2. **McGill, Brian J**; Rampal S. Etienne; John S. Gray and 15 other authors - "Species Abundance Distributions: moving beyond single prediction theories to integration within an ecological framework" (**Ecology Letters** 2007) 10:995-1015 (642 citations)
3. **McGill, Brian J**. – "Towards a unification of unified theories of biodiversity" (**Ecology Letters** 2010) 13(5):627-642 (129 citations)
4. Magurran, Anne and **Brian J. McGill** co-editors of "Biological diversity: frontiers in measurement and assessment" **Oxford University Press** 2010 (312 citations)
5. **McGill, Brian J** – "Matters of Scale" (**Science** 2010) 328(30 Apr):575-576 (132 citations)

Type of application: working group participant

Name: Isaac Austin Overcast
Nationality: United States of America
Address: 324 ½ E 8th St Apt #1A, New York, NY, 10009, USA
Fax: 1-212-650-8585
E-mail: iovercast@gc.cuny.edu
URL: <http://isaacovercast.com/>
Professional status: PhD-student

Education

2014-Present Ph.D. Student, Department of Biology
City College of New York & Graduate Center CUNY
1999 B.A./B.S., The Evergreen State College
..

Academic positions

N/A

..

General expertise (and its relevance for the working group if application is attached on working group)

Comparative phylogeography, Population Genetics, Community Assembly Modelling

Five important & for the project relevant publications (h-index= <...>, <...> citations/<date>)

Overcast I, Bagley J, Hickerson M (2017) *Improving approximate Bayesian computation tests for synchronous diversification by buffering divergence time classes*. In prep.

Overcast I, Hickerson M (2017) *Integrating island assembly models and comparative population genetics*. In prep.

Oswald, J. A., **Overcast, I.**, Mauck, W. M., Andersen, M. J., & Smith, B. T. (2017). *Isolation with asymmetric gene flow during the nonsynchronous divergence of dry forest birds*. Molecular Ecology.

Type of application: working group participant

Name: Christine Parent
Nationality: Canadian
Address: Department of Biological Sciences, University of Idaho, 875 Perimeter Drive MS 3051, Moscow ID 83844-3051
Fax: 208-885-7905
E-mail: ceparent@uidaho.edu
URL: <https://www.uidaho.edu/sci/biology/people/faculty/ceparent>

Professional status: Assistant professor

Education

2008 PhD (Evolutionary Biology) Simon Fraser University, Vancouver Canada
2000 MS (Evolutionary Biology) Carleton University, Ottawa Canada
1998 BS (Biology) McGill University, Montreal Canada

Academic positions

2013 - present Assistant Professor, University of Idaho, Dept. of Biological Sciences
2012 – 2013 Postdoctoral Fellow, University of California Berkeley
2008 – 2012 Postdoctoral Fellow, University of Texas at Austin

General expertise (and its relevance for the working group if application is attached on working group)

Evolution

Adaptive radiation

Biogeography

Community ecology

Five important & for the project relevant publications (h-index= 8, 455 citations/Feb 13, 2017)

Triantis KA, Rigal F, **Parent CE**, Cameron RAD, Lenzner B, Parmakelis A, Yeung NW, Alonso MR, Ibáñez M, Martins AMF, Teixeira DNF, Griffiths OL, Yanes Y, Hayes KA, Preece RC, Cowie RH (2016) Discordance between morphological and taxonomic diversity: land snails of oceanic archipelagos. *Journal of Biogeography* 43: 2050–2061

Parent CE, Agashe D, Bolnick DI (2014) Intraspecific competition reduces niche width in experimental populations. *Ecology & Evolution* 4(20):3978-3990.

Cameron RAD, Triantis KA, **Parent CE**, Alonso MR, Ibanez M, Martins AMF, Ladle RL, Whittaker RJ (2012) Snails on oceanic islands: testing the general dynamic model of oceanic island biogeography using linear mixed effect models. *Journal of Biogeography* 40:117–130.

Parent CE, Crespi BJ (2009) Ecological opportunity in adaptive radiation of Galapagos endemic land snails. *The American Naturalist* 174(6):898-905.

Parent CE, Caccone A, Petren K (2008) Colonization and diversification of Galápagos terrestrial fauna: a phylogenetic and biogeographical synthesis. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* 363:3347-3361.

Type of application: workshop participant

Name: James Rosindell
 Nationality: British
 Address: Imperial College London, Silwood Park Campus, Buckhurst Road, Ascot, Berkshire SL5 7PY, UK
 E-mail: j.rosindell@imperial.ac.uk
 URL: <http://www.imperial.ac.uk/people/j.rosindell>

Professional status: Research Fellow, Lecturer

Education

2005 University of Warwick, Mathematics.
 2008 University of Leeds, Zoology, Ph.D.

Academic positions

2008-2011 Postdoctoral research fellow, funded by the Engineering and Physical Sciences Research Council (EPSRC), hosted by the University of Leeds, spending extensive periods at the University of Groningen and the University of Idaho (Moscow, ID)
 2012 – present Research Fellow/Lecturer in Biodiversity Theory and Science Faculty of Natural Sciences, Department of Life Sciences (Silwood Park)

General expertise Biodiversity theorist with a particular interest in ecological neutral theory. Interested in questions such as, what are the factors influencing the presence of endemic species on islands? How many species will go extinct if an area of habitat is modified or destroyed. Approach to modeling problems in ecology is to search for simple models for observed phenomena if possible; a model does not have to explicitly reproduce reality in order to be useful. Most work uses simulation models and applies methods such as spatially explicit coalescence to maximise computational tractability. More specific research topics include: Ecological neutral theory; coalescence; island biogeography; habitat fragmentation; spatial patterns of biodiversity; phylogenetics; scientific data visualization.

Five important & relevant publications (h-index=14; i10-index= 19; 974 citations/2012)

- Rosindell, J. and Harmon, L.J., 2013. A unified model of species immigration, extinction and abundance on islands. *Journal of Biogeography*, 40(6), pp.1107-1118
- Rosindell, J., Hubbell, S.P., He, F., Harmon, L.J. and Etienne, R.S., 2012. The case for ecological neutral theory. *Trends in ecology & evolution*, 27(4), pp.203-208.
- Rosindell, James, and Albert B. Phillimore. 2011. A unified model of island biogeography sheds light on the zone of radiation." *Ecology letters* 14, no. 6, pp. 552-560.
- Rosindell, J., Hubbell, S.P. and Etienne, R.S., 2011. The unified neutral theory of biodiversity and biogeography at age ten. *Trends in ecology & evolution*, 26(7), pp.340-348.
- McInnes, L., Baker, W.J., Barraclough, T.G., Dasmahapatra, K.K., Goswami, A., Harmon, L.J., Morlon, H., Purvis, A., Rosindell, J., Thomas, G.H. and Turvey, S.T., 2011. Integrating ecology into macroevolutionary research. *Biology letters* 7 (5), 644-646

Type of application: working group applicant

Name:	Catherine E Wagner
Nationality:	American
Address:	University of Wyoming, Department of Botany, 1000 E University Ave, Laramie, WY USA
E-mail: catherine.wagner@uwyo.edu	
URL: www.cewagnerlab.com	
Professional status:	Assistant professor

Education

2011	PhD, Ecology and Evolutionary Biology, Cornell University
2004	BA, Biology-Geology, Whitman College

Academic positions

2015	Assistant Professor, Department of Botany, University of Wyoming
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General expertise (and its relevance for the working group if application is attached on working group)

Evolutionary adaptive radiation, evolutionary influences on communities

Five important & for the project relevant publications (h-index= 11, 1173 citations/February 9 2017)

Weber, M.G., **C.E. Wagner**, R.J. Best, L. Harmon, B. Matthews (2017) Evolution in a community context: on integrating ecological interactions and macroevolution. *Trends in Ecology & Evolution*, *in press*.

Wagner, C.E., L.J. Harmon, and O. Seehausen (2012) Ecological opportunity and sexual selection together predict adaptive radiation. *Nature*, 487:366-369.

Wagner, C. E., L. J. Harmon, O. Seehausen (2014) Cichlid species-area relationships are shaped by adaptive radiations that scale with area. *Ecology Letters*, 17:583-592.

Brawand, D.*, **Wagner, C. E.***, Li, Y. I.*, Malinsky, M., Keller, I., Fan, S., et al. (73 authors) (2014) The genomic substrate for adaptive radiation in African cichlid fish. *Nature*, 513(7518), 375–381.

Wagner, C.E., I. Keller, S. Wittwer, O.M. Selz, S. Mwaiko, L. Greuter, A. Sivasundar, O. Seehausen (2013) Genome-wide RAD sequence data provide unprecedented resolution of species boundaries and relationships in the Lake Victoria cichlid adaptive radiation. *Molecular Ecology*, 22:787-798.

Mike Hickerson

To: Rosemary Gillespie Cc: Andy Rominger

Re: sDiv call for Working Groups

January 9, 2017 at 5:56 AM

Important 

MH

Hello Rosie,

It sounds like a great plan! I hadn't heard about iDIV, but it looks like a great place. The only refinement I can think of could be plan #1 to include forward time community assembly models. ENMs/SDMs tend to be per taxon, but I have heard that there is increasing interest in pooled models.

1. Comparative phylogenetic and population genomic methods coupled with multi-taxa species distribution and community assembly models.

happy new year!

mike

On Jan 14, 2017, at 7:26 AM, Chase, Jonathan <jonathan.chase@idiv.de> wrote:

Hi Rosemary,

I am so sorry for the delay in my response. Anyway, if you're still interested in trying to pursue this, I'm totally up for it. I'm happy to dive in if you're still interested. Let me know if perhaps you might have time for a ~~skype?~~ |

Best,
Jon

Andy Rominger

To: Mike Hickerson Cc: Rosemary Gillespie

Re: sDiv call for Working Groups

January 9, 2017 at 10:38 AM

Important 

AR

Hi Rosie and Mike,

I'd be really excited to do this, sounds great! My time is limited now, as you pointed out Rosie, but if we could quickly turn the ideas in this email thread into the letter of intent, I'd be happy to be more involved in the actual drafting if the full proposal.

Harmon, Luke (lukeh@uidaho.edu)

To: Rosemary Gillespie Cc: Andy Rominger, Chase, Jonathan, Mike Hickerson

Re: sDiv proposal

January 17, 2017 at 2:45 PM

Important 

HL

Hi Rosie -

Thanks for including me in this, I really love it. In particular James Rosindell and I have been batting around the idea of a "double neutral" model that combines pop gen and ecological neutral theories together to make all sorts of new and strange predictions.

Incorporating macroecology, I think, can be accomplished by applying the techniques already outlined in the proposal to "macroecological" datasets - that is, I think we can weave that side of things in by adding perspectives on which data to analyze but keep the general framework the same.

Thanks-
Luke

[See More from Rosemary Gillespie](#)

Brent C Emerson

February 7, 2017 at 8:35 AM

To: Rosemary Gillespie

Re: sDiv proposal

BC

 New contact info found in this email: Brent C Emerson bemerson@ipna.csic.es

[add...](#)



Hi Rosie,

Thanks for thinking of me - sounds like a great opportunity, so count me in. I'll get back to you soon with the CV and dates.

All the best
Brent

Rampal S. Etienne 

Yesterday at 1:25 AM

RS

To: Rosemary Gillespie
Re: sDiv proposal

Dear Rosemary,

Thanks for the invitation. I'd be happy to be part of this although the fall (and particularly September) is full of teaching for me, so we'll have to see whether this would work. Also, I am part of another proposal, but I don't think that is necessarily conflicting (and I think I prefer this one!).

I have attached a CV. Please feel free to choose different publications from my pub list as you see fit.

I don't have all dates yet of the teaching I need to do, but November and December look most promising.

Cheers,

Rampal

[See More](#) from Rosemary Gillespie

--
Rampal S. Etienne
Associate professor
Groningen Institute for Evolutionary Life Sciences
Box 11103
9700 CC Groningen
The Netherlands

catherine.graham@wsl.ch

February 11, 2017 at 8:10 AM

To: Rosemary Gillespie Cc: Mike Hickerson, Catherine Graham

Re: sDiv proposal

Hi there!

You are right I missed your original proposal invitation - not sure why. But I would love to participate - the project sounds very interesting. I will send a CV tomorrow.

Thank you for considering me.

Catherine

Joaquin Hortal 

February 7, 2017 at 7:08 AM

To: Rosemary Gillespie

Re: sDiv proposal



Dear Rosie

Well, thanks a lot for thinking on me! The topic is really on the line of the research I've been moving towards over the last years, although between getting tenured, childcare and a number of PhD students I'm only managing to get fully into it this year. As you know, my weakest side there are evolutionary models, but I've been learning over the last years and can be of help there.

So yes, count me in. I'm certainly quite interested in participating. I'm quite tied these days, with a couple of deadlines and a PhD student handing in next wee. But please send the proposal trhough when you have a sensible draft. I know how things are with sDiv proposals, so don't worry if you can't make it on time for us to comment.

Also, let me know if you think the team may need some additional expertise to cover any particular aspect.

Re dates, currently I don't have anything settled yet for the end of the year. We use to spend a couple of months in Brazil between July and September, so for me it is better to keep it in the last quarter, but I could easily accommodate earlier in September, and this year we may not even go to Brazil, depending on several family issues. So please do pick an earlier date if it works better for the rest of participants.

Thanks again. And please find attached an updated CV in sDiv format.

All the best,

Joaquín

Petr Keil 

Today at 6:20 AM

To: Rosemary Gillespie

Re: sDiv proposal



Dear Rosemary,

It would be a pleasure, count me in.

Potential dates I could do: 10/2; 10/9; 10/16; 10/23; 10/30; 11/6; 11/13; 11/20; 11/27; 12/4; 12/11

The CV is attached.

I am looking forward to hearing more about that.

Yours,

Petr

Knight, Tiffany Marie 

Today at 5:43 PM



To: Rosemary Gillespie

Re: sDiv proposal

Dear Rosemary,

I would be delighted to join. Thank you for thinking of me. I am sorry it took my so long to respond. I was ill and then traveling.

My cv is attached in the idiv format.

I am not available the weeks of 10/9; 10/16. Any of the other weeks could work for me.

Best,

Tiffany

Luke Mahler

February 6, 2017 at 7:47 PM

To: Rosemary Gillespie

Re: sDiv proposal

LM

 New contact info found in this email: Luke Mahler luke.mahler@utoronto.ca

[add...](#)

(X)

Hi Rosie,

This sounds great - I'm very much interested.

I had a great conversation with Jon Chase about these sorts of questions in December, and I'd love to be part of the group.

I'm pretty slammed this week but can get you the CV no problem. Happy to provide input on other stuff if you'd like, although it'll probably be tough for me to provide heavy writing or edits this week.

As for dates, I can definitely do 11/6 and 12/11.

Most likely I can do any of the dates except for 8/28, but there's a chance I'll teach in the fall, which would make the above dates preferable. Even if I teach this fall I could escape for a week if necessary, so don't worry too much if other dates are preferable.

Thanks for the invite - sounds really exciting!

Best,
Luke

FM

Francois Massol 

February 7, 2017 at 1:19 AM

To: Rosemary Gillespie

RE: sDiv proposal

Dear Dr. Gillespie,

I feel very honored to have been invited to participate in this workshop. I am indeed very much interested by the topic you propose and I hope to be able to contribute to the making of the models mentioned in the abstract (especially if it is possible to make a connection between the trophic theory of island biogeography model I developed with Dominique Gravel and the macro-evolutionary models you seem to have in mind).

Please find attached my CV – I think all items are filled, but maybe some polishing/formatting is required as I was not exactly sure about the expectations for some of the items.

Regarding availability, the following weeks could work for me:

8/28, 9/11, 9/25, 10/30, 11/13, 11/27, 12/11

I'll try to answer with more constructive comments in a few days – my schedule is awfully busy until Thursday because of the ERC consolidator deadline.

Best,

AM

Angela McGaughran 

Yesterday at 6:05 PM

To: Rosemary Gillespie

Inbox - gillespie@berkeley.edu 

Re: Invitation to be part of sDiv proposal



Hi again Rosemary,

Please find a one-page CV attached. I wasn't too sure what to put for the 'general expertise' and 'publications' sections, so please have a look and let me know what you think (e.g., I have some more recent publications - see my google scholar profile if you like - but I tried to pick the most relevant as suggested). Happy to change/adapt anything if you think it would be more suitable.

Thanks for the invitation to be a part of this exciting work!

All the best,

Angela

[See More from Rosemary Gillespie](#)

Dr. Angela McGaughran
DECRA Fellow
Australian National University
Research School of Biology
Evolution, Ecology and Genetics
Canberra ACT 2601
Australia

To: Rosemary Gillespie

Re: sDiv proposal

BM

Hi Rosemary,

This sounds like an exciting proposal. I would like to be a part of it but my plans are a bit uncertain as I am due for a sabbatical this fall and am still discussing plans with family and awaiting to hear from fellowships. That said, if I end up in Europe (a good chance as Montpellier is a place I am looking at) or stay put in Maine I think I should be able to make this. I guess if I end up in South America it might be harder to justify. Can I give you an 80% yes for now with permission to include me in the application?

My CV is attached. Since I may be moving family internationally for the semester, dates not in the first three weeks or last two weeks of your list would be best for me but conversely am wide open in the middle.

Brian

isaac overcast

To: Rosemary Gillespie

Re: sDiv proposal

February 7, 2017 at 2:47 PM

IO

Hey Rosie!

Nice to hear from you! Yes, Mike has been telling me about this workshop and I would be absolutely thrilled to participate! It sounds like really great fun, nice company, and very interesting material. So yes, I am totally in, thank you for considering me. As for the CV I will fill out this form and return it within the next day or two.

All the dates you listed work for me _except_ the week beginning 9/11, other than that I'm totally available.

Also, I heard you bumped into my friend Sara Lipshutz recently at a conference in Switzerland, if I recall correctly. She's a good friend of mine. Very small world!

hope alls well, very nice to hear from you,

-isaac

Parent, Christine (ceparent@uidaho.edu)

February 7, 2017 at 9:19 AM

PC

To: Rosemary Gillespie

Re: sDiv proposal

 New contact info found in this email: Christine Parent ceparent@uidaho.edu

[add...](#)[\(X\)](#)

Hi Rosie,

It is very nice to hear from you! This is a timely topic for a working group and you have assembled quite the team. I am definitively interested in participating. I have a full day but I will send you my formatted CV, dates that could work for me, and input on the abstract later today. All the application requires is an abstract or do you have a more developed proposal for the working group?

Very best wishes,
Christine

From: "Catherine E. Wagner" <Catherine.Wagner@uwyo.edu>

Subject: Re: sDiv proposal

Date: February 6, 2017 at 4:43:51 PM PST

To: Rosemary Gillespie <gillespie@berkeley.edu>

Cc: "Catherine E. Wagner" <Catherine.Wagner@uwyo.edu>

Dear Rosemary,

Great to hear from you! I'd love to be involved as these are topics I'm really seeking to work on more in several systems.

I will get a CV in the requested format together, and feel free to send along the proposal if you'd like my feedback. I should be able to have a quick look through prior to Feb 15th.

Wonderful you got to spend some time in Switzerland at the Biology meeting!

Best,
Katie

Catherine Wagner
Assistant Professor
Biodiversity Institute and Department of Botany
University of Wyoming

email: catherine.wagner@uwyo.edu
website: www.cewagnerlab.com